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sequences shown in Fig. 1

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taggcacaaa ctttatagat gtaggcggct tactcggtta tcttcaaatt ggtttaattg    4860

aaacaattcc attcgacggt ttgtgtttcc tcatttcgga ggcgacattt cttgtaacaa    4920

atgtatcaat aagaagttgt ctagaaagtg ataaaacatc agcagagagt tgtggcgtag    4980

tacgtctgtt cttcaacacg taagtcattg atgtccaaat cgaggtatgg agtagttcta    5040

aaaatatcgg agccataaga acttgtaatg tcggtaaagt tctcctctaa catctcatgg    5100

tataaggcac aatcccagct taggtaacag gttttggat aaatctctac gtaacagtaa    5160

taggtactat cggagtgtct gcatatacat tcggtagaac ttacatatta aaacaacaaa    5220

agttgttggc gagcacttgt cgaagatatg aaaaagtaaa agaagtacta attatatcaa    5280

atgccttata ttcatatgtt tttcaaatat cattagagta ttatagactt tgtgtatgta    5340

ttttgtacct tcttaatgtg ctacagcaac tctatttacc gaaaaataac agtatcaaat    5400

gtttaagcgt cattagaagt agaaaatgct tataacgtct tagacaaaat aggttggtca    5460

ctaaaaacat attatattga ccataggata gaaggctatc ttacgacaat aaattgtaaa    5520

aacgtggata attcaatgta gacagtttag gtagaaaggt tgactgaaat acattgctac    5580
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gctttatcgt aaatagtgat acagcatggg ttaatagtac tgttctaaga gaatttatgc    5640

attagaataa tagagaacgt ataagcatta tcattaacat ttctcatatg ctattgtcat    5700

atctatatgt gcactatatt tataaattgg ggtaaggact cattttatta atgctataat    5760

gtaaaggaaa ataataaaaa tacaaaatca ataaacaatc caatatgttt ttaatacaaa    5820

taaacacata taaatttcgc agcaattctt attcgaatca attgtataat agcgaatcca    5880

aaacatcata aacttaggaa agaaatttac ctaataaaaa ggttacgtat aaatatcgaa    5940

gtaggtttca tattgtaaat tgtaagtctt aacgccggcg ttaagttaag cattagtacc    6000

agtatcgaca aaggacacac tttaacaata ggcgagtgtt aaggtgtgtt gtatgctcgg    6060

ccttcgtatt tcacatttcg daccccacgg attactcact cgattgagtg taattaacgc    6120

aacgcgagtg acgggcgaaa ggtcagccct ttggacagca cggtcgacgt aattacttag    6180

ccggttgcgc gcccctctcc gccaaacgca taacccgcga gaaggcgaag gagcgagtga    6240

ctgagcgacg cgagccagca agccgacgcc gctcgccata gtcgagtgag tttccgccat    6300

tatgccaata ggtgtcttag tcccctattg cgtcctttct tgtacactcg ttttccggtc    6360

gttttccggt ccttggcatt tttccggcgc aacgaccgca aaaggtatc cgaggcgggg     6420

ggactgctcg tagtgttttt agctgcgagt tcagtctcca ccgctttggg ctgtcctgat    6480

atttctatgg tccgcaaagg gggaccttcg agggagcacg cgagaggaca aggctgggac    6540

ggcgaatggc ctatggacag gcggaaagag ggaagccctt cgcaccgcga aagagtatcg    6600

agtgcgacat ccatagagtc aagccacatc cagcaagcga ggttcgaccc gacacacgtg    6660

cttggg gggc aagtcgggct ggcgacgcgg aataggccat tgatagcaga actcaggttg    6720

ggccattctg tgctgaatag cggtgaccgt cgtcggtgac cattgtccta atcgtctcgc    6780

tccatacatc cgccacgatg tctcaagaac ttcaccaccg gattgatgcc gatgtgatct    6840

tcctgtcata aaccatagac gcgagacgac ttcggtcaat ggaagccttt ttctcaacca    6900

tcgagaacta ggccgtttgt ttggtggcga ccatcgccac caaaaaaaca aacgttcgtc    6960

gtctaatgcg cgtctttttt tcctagagtt cttctaggaa actagaaaag atgccccaga    7020

ctgcgagtca ccttgctttt gagtgcaatt ccctaaaacc agtactctaa tagtttttcc    7080

tagaagtgga tctaggaaaa tttaattttt acttcaaaat ttagttagat ttcatatata    7140

ctcatttgaa ccagactgtc aatggttacg aattagtcac tccgtggata gagtcgctag    7200

acagataaag caagtaggta tcaacggact gaggggcagc acatctattg atgctatgcc    7260

ctcccgaatg gtagaccggg gtcacgacgt tactatggcg ctctgggtgc gagtggccga    7320
```

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ggtctaaaata gtcgttattt ggtcggtcgg ccttcccggc tcgcgtcttc accaggacgt      7380

tgaaataggc ggaggtaggt cagataatta acaacggccc ttcgatctca ttcatcaagc      7440

ggtcaattat caaacgcgtt gcaacaacgg taacgatgtc cgtagcacca cagtgcgagc      7500

agcaaaccat accgaagtaa gtcgaggcca agggttgcta gttccgctca atgtactagg      7560

gggtacaaca cgttttttcg ccaatcgagg aagccaggag gctagcaaca gtcttcattc      7620

aaccggcgtc acaatagtga gtaccaatac cgtcgtgacg tattaagaga atgacagtac      7680

ggtaggcatt ctacgaaaag acactgacca ctcatgagtt ggttcagtaa gactcttatc·     7740

acatacgccg ctggctcaac gagaacgggc cgcagttatg ccctattatg gcgcggtgta      7800

tcgtcttgaa attttcacga gtagtaacct tttgcaagaa gccccgcttt tgagagttcc      7860

tagaatggcg acaactctag gtcaagctac attgggtgag cacgtgggtt gactagaagt      7920

cgtagaaaat gaaagtggtc gcaaagaccc actcgttttt gtccttccgt tttacggcgt      7980

ttttttcctt attcccgctg tgcctttaca acttatgagt atgagaagga aaaagttata      8040

ataacttcgt aaatagtccc aataacagag tactcgccta tgtataaact tacataaatc      8100

tttttatttg tttatcccca aggcgcgtgt aaagggctt· ttcacggtgg actgcagatt      8160

ctttggtaat aatagtactg taattggata tttttatccg catagtgctc                 8210


<210>    4
<211>    2100
<212>    DNA
<213>    Artificial

<220>
<223>    mCEA(6D) sequence shown in Fig. 2A

<400>    4
atggagtctc cctcggcccc tccccacaga tggtgcatcc cctggcagag gctcctgctc       60

acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc      120

acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag      180

catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata      240

ggatatgtaa taggaactca acaagctacc ccagggcccg catacagtgg tcgagagata      300

atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac      360

accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta      420

tacccggaac tccctaagcc ttctattagc tccaataata gtaagcctgt cgaagacaaa      480
```

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gatgccgtcg cttttacatg cgagcccgaa actcaagacg caacatatct ctggtgggtg    540

aacaaccagt ccctgcctgt gtccctaga ctccaactca gcaacggaaa tagaactctg    600

accctgttta acgtgaccag gaacgacaca gcaagctaca aatgcgaaac ccaaaatcca    660

gtcagcgcca ggaggtctga ttcagtgatt ctcaacgtgc tttacggacc cgatgctcct    720

acaatcagcc ctctaaacac aagctataga tcaggggaaa atctgaatct gagctgtcat    780

gccgctagca atcctcccgc ccaatacagc tggtttgtca atggcacttt ccaacagtcc    840

acccaggaac tgttcattcc caatattacc gtgaacaata gtggatccta cacgtgccaa    900

gctcacaata gcgacaccgg actcaaccgc acaaccgtga cgacgattac cgtgtatgag    960

ccaccaaaac cattcataac tagtaacaat tctaacccag ttgaggatga ggacgcagtt   1020

gcattaactt gtgagccaga gattcaaaat accacttatt tatggtgggt caataaccaa   1080

agtttgccgg ttagcccacg cttgcagttg tctaatgata ccgcacatt gacactcctg   1140

tccgttactc gcaatgatgt aggaccttat gagtgtggca ttcagaatga attatccgtt   1200

gatcactccg accctgttat ccttaatgtt ttgtatggcc cagacgaccc aactatatct   1260

ccatcataca cctactaccg tcccggcgtg aacttgagcc tttcttgcca tgcagcatcc   1320

aacccccctg cacagtactc ctggctgatt gatggaaaca ttcagcagca tactcaagag   1380

ttatttataa gcaacataac tgagaagaac agcggactct atacttgcca ggccaataac   1440

tcagccagtg gtcacagcag gactacagtt aaaacaataa ctgtttccgc ggagctgccc   1500

aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc   1560

acctgtgaac ctgaggctca gaacacaacc tacctgtggt gggtaaatgg tcagagcctc   1620

ccagtcagtc ccaggctgca gctgtccaat ggcaacagga ccctcactct attcaatgtc   1680

acaagaaatg acgcaagagc ctatgtatgt ggaatccaga actcagtgag tgcaaaccgc   1740

agtgacccag tcaccctgga tgtcctctat gggccggaca cccccatcat ttcccccccca   1800

gactcgtctt acctttcggg agcggacctc aacctctcct gccactcggc ctctaaccca   1860

tccccgcagt attcttggcg tatcaatggg ataccgcagc aacacacaca agttctcttt   1920

atcgccaaaa tcacgccaaa taataacggg acctatgcct gttttgtctc taacttggct   1980

actggccgca ataattccat agtcaagagc atcacagtct ctgcatctgg aacttctcct   2040

ggtctctcag ctggggccac tgtcggcatc atgattggag tgctggttgg ggttgctctg   2100


<210>   5
<211>   2100
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<212> DNA
<213> Artificial

<220>
<223> mCEA(6D, 1st & 2nd) sequence shown in Fig. 2A

<400> 5
atggagtctc cctcggcccc tccccacaga tggtgcatcc cctggcagag gctcctgctc   60

acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc   120

acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag   180

catcttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata   240

ggatatgtaa taggaactca caagctacc ccagggcccg catacagtgg tcgagagata   300

atataccccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac   360

accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta   420

tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaacccgt ggaggacaag   480

gatgctgtgg ccttcacctg tgaacctgag actcaggacg caacctacct gtggtgggta   540

aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc   600

actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca   660

gtgagtgcca ggcgcagtga ttcagtcatc ctgaatgtcc tctatggccc ggatgccccc   720

accatttccc ctctaaacac atcttacaga tcaggggaaa atctgaacct ctcctgccac   780

gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc   840

acccaagagc tctttatccc caacatcact gtgaataata gtggatccta tacgtgccaa   900

gcccataact cagacactgg cctcaatagg accacagtca cgacgatcac agtctatgag   960

ccacccaaac ccttcatcac cagcaacaac tccaacccccg tggaggatga ggatgctgta   1020

gccttaacct gtgaacctga gattcagaac acaacctacc tgtggtgggt aaataatcag   1080

agcctcccgg tcagtcccag gctgcagctg tccaatgaca acaggaccct cactctactc   1140

agtgtcacaa ggaatgatgt aggaccctat gagtgtggaa tccagaacga attaagtgtt   1200

gaccacagcg acccagtcat cctgaatgtc ctctatggcc cagacgaccc caccatttcc   1260

ccctcataca cctattaccg tccaggggtg aacctcagcc tctcctgcca tgcagcctct   1320

aacccacctg cacagtattc ttggctgatt gatgggaaca tccagcaaca cacacaagag   1380

ctctttatct ccaacatcac tgagaagaac agcggactct atacctgcca ggccaataac   1440

tcagccagtg ccacagcag gactacagtc aagacaatca cagtctctgc ggagctgccc   1500

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aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc    1560

acctgtgaac ctgaggctca gaacacaacc tacctgtggt gggtaaatgg tcagagcctc    1620

ccagtcagtc ccaggctgca gctgtccaat ggcaacagga ccctcactct attcaatgtc    1680

acaagaaatg acgcaagagc ctatgtatgt ggaatccaga actcagtgag tgcaaaccgc    1740

agtgacccag tcaccctgga tgtcctctat gggccggaca cccccatcat ttcccccccca    1800

gactcgtctt acctttcggg agcggacctc aacctctcct gccactcggc ctctaaccca    1860

tccccgcagt attcttggcg tatcaatggg ataccgcagc aacacacaca agttctcttt    1920

atcgccaaaa tcacgccaaa taataacggg acctatgcct gttttgtctc taacttggct    1980

actggccgca ataattccat agtcaagagc atcacagtct ctgcatctgg aacttctcct    2040

ggtctctcag ctggggccac tgtcggcatc atgattggag tgctggttgg ggttgctctg    2100
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<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6

Leu Leu Thr Phe Trp Asn Pro Pro Thr
1   5

<210> 7
<211> 10
<212> PRT
<213> Homo sapiens

<400> 7

Val Leu Tyr Gly Pro Asp Ala Pro Thr Ile
1   5   10

<210> 8
<211> 9
<212> PRT
<213> Homo sapiens

<400> 8

Ile Met Ile Gly Val Leu Val Gly Val
1   5

<210> 9
<211> 9
<212> PRT
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<213> Homo sapiens

<400> 9

Gln Ile Ile Gly Tyr Val Ile Gly Thr
1               5


<210> 10
<211> 9
<212> PRT
<213> Homo sapiens

<400> 10

Lys Thr Cys Pro Val Gln Leu Trp Val
1               5


<210> 11
<211> 9
<212> PRT
<213> Homo sapiens

<400> 11

Ser Thr Pro Pro Pro Gly Thr Arg Val
1               5


<210> 12
<211> 11
<212> PRT
<213> Homo sapiens

<400> 12

Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu
1               5                   10


<210> 13
<211> 10
<212> PRT
<213> Homo sapiens

<400> 13

Val Val Val Pro Tyr Glu Pro Pro Glu Val
1               5                   10


<210> 14
<211> 314
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1               5                   10                  15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
            20                  25                  30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
        35                  40                  45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
    50                  55                  60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65                  70                  75                  80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
                85                  90                  95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
            100                 105                 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
        115                 120                 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
    130                 135                 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145                 150                 155                 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                165                 170                 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
            180                 185                 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
        195                 200                 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
    210                 215                 220

```
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225             230             235             240


Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
             245             250             255


Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
             260             265             270


Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
             275             280             285


Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
    290             295             300


Met Gly Glu Met His Arg Glu Leu Asn Ala
305             310


<210>   15
<211>   314
<212>   PRT
<213>   Artificial

<220>
<223>   Modified KSA amino acid sequence as shown in Fig. 3

<400>   15

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
.1          5               10              15


Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
             20              25              30


Lys Leu Ala Val Asn Cys Phe Val Asn Asn Arg Gln Cys Gln Cys   .
         35              40              45


Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
    50              55              60


Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65              70              75              80


Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
             85              90              95
```

```
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
            100             105             110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
            115             120             125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
            130             135             140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145             150             155             160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
                165             170             175

Asp Pro Lys Phe Ile Thr Ser Val Leu Tyr Glu Asn Asn Val Ile Thr
            180             185             190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
            195             200             205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
    210             215             220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225             230                 235             240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
                245             250             255

Pro Glu Phe Ser Met Gln, Gly Leu Lys Ala Gly Val Ile Ala Val Ile
            260             265             270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
            275             280             285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
    290             295             300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305             310
```

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<210>  16
<211>  10
<212>  PRT
<213>  Homo sapiens

<400>  16

Gln Leu Asp Pro Lys Phe Ile Thr Ser Ile
1               5                   10


<210>  17
<211>  10
<212>  PRT
<213>  Artificial

<220>
<223>  Amino acid sequence of KSA peptide modified at amino acid 10

<400>  17

Gln Leu Asp Pro Lys Phe Ile Thr Ser Val
1               5                   10


<210>  18
<211>  36
<212>  DNA
<213>  Homo sapiens

<400>  18
caaaatttat cacgagtgtg ttgtatgaga ataatg                        36


<210>  19
<211>  36
<212>  DNA
<213>  Artificial

<220>
<223>  Nucleotide sequence of KSA peptide modified at amino acid 10

<400>  19
cattattctc atacaacaca ctcgtgataa attttg                        36


<210>  20
<211>  945
<212>  DNA
<213>  Artificial

<220>
<223>  Modified KSA nucleic acid sequence as shown in Fig. 3B

<400>  20
atggcgcccc cgcaggtcct cgcgttcggg cttctgcttg ccgcggcgac ggcgactttt     60
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gccgcagctc aggaagaatg tgtctgtgaa aactacaagc tggccgtaaa ctgctttgtg   120

aataataatc gtcaatgcca gtgtacttca gttggtgcac aaaatactgt catttgctca   180

aagctggctg ccaaatgttt ggtgatgaag gcagaaatga atggctcaaa acttgggaga   240

agagcaaaac ctgaaggggc cctccagaac aatgatgggc tttatgatcc tgactgcgat   300

gagagcgggc tctttaaggc caagcagtgc aacggcacct ccacgtgctg gtgtgtgaac   360

actgctgggg tcagaagaac agacaaggac actgaaataa cctgctctga gcgagtgaga   420

acctactgga tcatcattga actaaaacac aaagcaagag aaaaacctta tgatagtaaa   480

agtttgcgga ctgcacttca gaaggagatc acaacgcgtt atcaactgga tccaaaattt   540

atcacgagtg tgttgtatga gaataatgtt atcactattg atctggttca aaattcttct   600

caaaaaactc agaatgatgt ggacatagct gatgtggctt attattttga aaaagatgtt   660

aaaggtgaat ccttgtttca ttctaagaaa atggacctga cagtaaatgg ggaacaactg   720

gatctggatc ctggtcaaac tttaatttat tatgttgatg aaaaagcacc tgaattctca   780

atgcagggtc taaaagctgg tgttattgct gttattgtgg ttgtggtgat agcagttgtt   840

gctggaattg ttgtgctggt tatttccaga aagaagagaa tggcaaagta tgagaaggct   900

gagataaagg agatgggtga gatgcatagg gaactcaatg cataa   945

<210>   21
<211>   9515
<212>   DNA
<213>   Artificial

<220>
<223>   Sense strand of plasmid pT225KSAV-1 shown in Fig. 5

<400>   21
atggcgcccc cgcaggtcct cgcgttcggg cttctgcttg ccgcggcgac ggcgactttt   60

gccgcagctc aggaagaatg tgtctgtgaa aactacaagc tggccgtaaa ctgctttgtg   120

aataataatc gtcaatgcca gtgtacttca gttggtgcac aaaatactgt catttgctca   180

aagctggctg ccaaatgttt ggtgatgaag gcagaaatga atggctcaaa acttgggaga   240

agagcaaaac ctgaaggggc cctccagaac aatgatgggc tttatgatcc tgactgcgat   300

gagagcgggc tctttaaggc caagcagtgc aacggcacct ccacgtgctg gtgtgtgaac   360

actgctgggg tcagaagaac agacaaggac actgaaataa cctgctctga gcgagtgaga   420

acctactgga tcatcattga actaaaacac aaagcaagag aaaaacctta tgatagtaaa   480

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agtttgcgga ctgcacttca gaaggagatc acaacgcgtt atcaactgga tccaaaattt     540

atcacgagtg tgttgtatga gaataatgtt atcactattg atctggttca aaattcttct     600

caaaaaactc agaatgatgt ggacatagct gatgtggctt attattttga aaaagatgtt     660

aaaggtgaat ccttgtttca ttctaagaaa atggacctga cagtaaatgg ggaacaactg     720

gatctggatc ctggtcaaac tttaatttat tatgttgatg aaaaagcacc tgaattctca     780

atgcagggtc taaaagctgg tgttattgct gttattgtgg ttgtggtgat agcagttgtt     840

gctggaattg ttgtgctggt tatttccaga aagaagagaa tggcaaagta tgagaaggct     900

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